

TABLE 1

SEQ ID NO	Template ID	Clone ID	GenBank ID	E-value	Annotation	D.E. (log2)
1	980547.1	4764233	g3511023	8.00E-06	GAGE-8 [Homo sapiens]	3.45
2	4030354CB1	2511379	g3511027	2.00E-68	GAGE-7B [Homo sapiens]	2.51
3	3886578CB1	5298447	g35184	5.00E-56	p27 [Homo sapiens]	2.08
4	1471808CB1	3074415	g533523	0	MAGE-6 antigen [Homo sapiens]	1.74
5	3094768CB1	322569	g1177476	4.00E-67	interferon-inducible protein [Homo sapiens]	1.62
6	1097797.1	2507719	g533528	0	MAGE-9 antigen [Homo sapiens]	1.57
7	476210.8	1707023	g887922	4.00E-67	interferon-inducible peptide precursor [Homo sapiens]	1.56
8	236484.15	1922233	g2281071	0	transcription factor ISGF-3 [Homo sapiens]	1.49
9	050715.3	1425686	g5926694	0	HLA Class I region, chromosome 6p21.3, section 6/20 [Homo sapiens]	1.40
10	197880.1	2416222	g6453516	5.00E-43	hypothetical protein [Homo sapiens]	1.33
11	064516CB1	1304365	g3511023	2.00E-23	GAGE-8 protein [Homo sapiens]	2.67
12	347492.1	6024084	g8216987	2.00E-20	putative tumor antigen [Homo sapiens]	2.57
13	236992.2	636350	g854326	0	semaphorin B [Mus musculus]	1.92
14	213413.1	3572058			Incite Unique	2.10
15	032481.1	4073339			Incite Unique	1.76
16	428822.1	5322134	g5926699	7.00E-11	HLA Class I region, chromosome 6p21.3 [Homo sapiens]	1.67
17	898547.1	3003255	g4995817	5.00E-05	proline rich synapse associated protein 1 [Rattus norvegicus]	1.66
18	231486.18	1919287	g1359443	3.00E-81	hepatitis C-associated microtubular aggregate protein p44 [Homo sapiens]	1.53
19	409895.3	2060823	g36178	3.00E-47	S100P calcium-binding protein [Homo sapiens]	-1.34
20	3732868CB1	1217764	g182851	1.00E-49	G0S2 protein [Homo sapiens]	-1.41
21	2110909CB1	2605935	g165009	0	progesterone-induced protein [Oryctolagus cuniculus]	-1.42
22	1166265.1	759508	g2661752	0	phosphoenolpyruvate carboxykinase [Homo sapiens]	-1.72
23	3346307CB1	3120209	g7020645	1.00E-130	unnamed protein product [Homo sapiens]	-1.74
24	406992.1	4413637	g5668545	1.00E-167	cystine/glutamate transporter [Homo sapiens]	-1.81
25	200578.1	473724			Incite Unique	1.63

TABLE 2

SEQ ID NO	Template ID	Clone ID	Start	Stop
1	980547.1	4764233	1	628
2	4030354CB1	2511379	44	581
3	3886578CB1	5298447	5	629
4	1471808CB1	3074415	1	501
5	3094768CB1	322569	241	781
6	1097797.1	2507719	473	1659
7	476210.8	1707023	1	411
8	236484.15	1922533	3229	4192
9	050715.3	1425686	1	519
10	197880.1	2416222	758	1713
11	064516CB1	1304365	63	514
12	347492.1	6024084	45	769
13	236992.2	636350	2744	3197
14	213413.1	3572058	141	539
15	032481.1	4073339	937	1338
16	428822.1	5322134	1	658
17	898547.1	3003255	109	1193
18	231486.18	1919287	1684	2083
19	409895.3	2060823	397	810
20	3732868CB1	1217764	266	922
21	2110909CB1	2605935	1059	2148
22	1166265.1	759508	2032	2449
23	3346307CB1	3120209	12	1696
24	406992.1	4413637	1	922
25	200578.1	473724	1662	2308

TABLE 3

SEQ ID NO	Template ID	Start	Stop	Frame	Pfam ID	Pfam Description	E-value
4	1471808CB1	226	912	forward 1	MAGE	MAGE family	4.00E-135
6	1097797.1	1338	2022	forward 1	MAGE	MAGE family	9.80E-144
8	236484.15	2016	2216	forward 3	SH2	Src homology domain 2	8.00E-11
8	236484.15	300	2015	forward 3	STAT	STAT protein	0
13	236992.2	390	1634	forward 3	Sema	Sema domain	3.80E-181
17	898547.1	116	307	forward 2	SAM	SAM domain (Sterile alpha motif)	2.60E-07
19	409895.3	357	441	forward 1	efhand	EF hand	1.80E-04
19	409895.3	208	339	forward 1	S_100	S-100/ICaBP type calcium binding domain	2.70E-21
21	2110909CB1	114	1136	forward 3	aminotran_5	Aminotransferases class-V	3.00E-126
22	1166265.1	495	2279	forward 3	PEPCK	Phosphoenolpyruvate carboxykinase	0